Amendments to the Specification

Please replace the paragraph at page 5, lines 20-23 with the following:

Figure 7 shows the transient difference spectrum (25 μs subsequent to photolysis) overlaid with the equilibrium difference spectrum (deoxy minus CO-bound) for HemAT-*Hs* (Figure 7A, top panel) and HemAT-*Bs* (Figure 7B, bottom panel). Sample conditions are as described in Figure 4.

Please replace the paragraph at page 5, lines 24-27 with the following:

Figure 8 provides CO-off rate data for HemAT-*Hs* (dashed line), HemAT-*Bs* (dotted line), and horse heart Mb (solid line). Changes in absorbance as a function of time at 418 were monitored after the addition of potassium ferricyanide (final concentration of 1.5 mM). See Example ~~17~~ 16 for details.

Please replace the paragraph at page 35, line 29 to page 36, line 5 with the following:

Figure 6 displays typical transient absorption data subsequent to CO photolysis obtained at 430 nm at 25°C and 1 atm CO for both HemAT-*Hs* (solid line) and HemAT-*Bs* (dotted line). The data can be fit to a single exponential decay indicating a pseudo-first order reaction with CO. The resulting rate constant for CO recombination are found to be 30±3 s^{-1} and 132±3 s^{-1} for HemAT-Hs and HemAT-*Bs*, respectively. ~~Figure 7 shows~~ Figures 7A-B show the corresponding transient difference spectrum (25 μs subsequent to photolysis) overlaid with the equilibrium difference spectrum (deoxy minus CO-bound) for HemAT-*Hs* (Figure 7A, top panel) and HemAT-*Bs* (Figure 7B, bottom panel). The red-shift in the transient difference spectra relative to the equilibrium difference spectra suggest that CO photolysis produces a non-equilibrium five-coordinate complex within 25 μs subsequent to photolysis.

Please replace the paragraph at page 12, lines 20-28 with the following:

The report of myoglobin-type aerotaxis proteins in microorganisms, and the recent discovery of HemAT-*Hs* and HemAT-*Bs* has prompted an effort to find one or more signature motifs in these possible microbial globins. These would identify conserved regions

of the proteins. In addition, with these motifs in hand, contemporary computer algorithms like those contained in the BLAST programs ~~(http://www.ncbi.nlm.nih.gov/BLAST/)~~ could permit convenient and rapid searches for other possible globins using this signature motif. These motifs could be used for classifying these newly discovered microbial globins together and eventually with the whole globin family.

Please replace the paragraph at page 13, lines 9-31 with the following (but note that the underlined text appeared in the original and does not reflect the addition of matter):

An 80-aa consensus peptide sequence was constructed using the manual alignment of sperm whale myoglobin (SWMb), the oxygen sensor in *Bacillus subtilis*, HemAT-*Bs*, and the oxygen sensor in *Halobacterium salinarum*, HemAT-*Hs*. The intent was to find a minimal length of protein containing the myoglobin signature motif and see how many myoglobin proteins this sequence would recognize on the non-redundant (nr) database at NIH using the BLAST server ~~(http://www.ncbi.nlm.nih.gov/BLAST/)~~. An X was issued to residues of high variability (Bashford et al., "Determinants of a Protein Fold: Unique Features of the Globin Amino Acid Sequences," J. Mol. Biol., 196:199-216 (1987), which is hereby incorporated by reference) while conserved residues retained their specific amino acid designation. Critical to the alignment was the positioning of the two residues known to be absolutely conserved in all known globins: Phe at the CD1 position and the proximal His at the F8 position (Bashford et al., "Determinants of a Protein Fold: Unique Features of the Globin Amino Acid Sequences," J. Mol. Biol., 196:199-216 (1987), which is hereby incorporated by reference). Using these residues as markers, the myoglobin-like protein (MbLP) sequence was generated and consisted of two domains separated by 32 variable amino acids. The first myoglobin-type domain (M1-box) contained the absolutely conserved phenylalanine residue; the second (M2-box) contained the absolutely conserved proximal histidine. A BLAST search was then performed, comparing the sequences of MbLP and SWMb with those of all other proteins in the non-redundant database. Search parameters were default except for the EXPECT parameter, which was increased to 1000 to allow for matches of lesser sequence homology. This comparison between the number and type of SWMb hits and MbLP hits was used to assess the quality of the MbLP sequence in extracting myoglobin proteins.